

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/747, 994 A
Source: IFW/6
Date Processed by STIC: 09/14/2006

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 09/14/2006

PATENT APPLICATION: US/10/747,994A

TIME: 10:16:44

Input Set : A:\USAV2003-0073USNP-Sequence-AUG2006.ST25.txt

Output Set: N:\CRF4\09142006\J747994A.raw

3 <110> APPLICANT: Aventis Pharmaceuticals Inc.
 4 PARKAR, Ashfaq
 5 AUGUST, Paul
 6 KUNTZWEILER, Theresa
 7 ARDATI, Mohamad Ali
 8 BASKARAN, Namadev
 10 <120> TITLE OF INVENTION: Nucleic Acid Encoding A Novel Prostaglandin Receptor Protein
 And
 11 Methods of Use Thereof
 13 <130> FILE REFERENCE: USAV2003/0073 US NP
 15 <140> CURRENT APPLICATION NUMBER: 10/747,994A
 16 <141> CURRENT FILING DATE: 2003-12-30
 18 <160> NUMBER OF SEQ ID NOS: 18
 20 <170> SOFTWARE: PatentIn version 3.3
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1038
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Cavia porcellus
 27 <400> SEQUENCE: 1
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 30 ggcgagtgct tcttcagcgc gggcctcctg ggcaacctgc tggccctagc gctgctggca 120
 32 cgctcggggc tcgggtcctg ccggccgcgc ccgcagccct cagtcttcta cgtgctggtg 180
 34 tgcggcttga cggtcacaga cctgctagga aagtgcctgg tgagcccggg ggtgctggct 240
 36 gcctatgcgc aaaaccggag cctcagggga ctggcaccgc cgcagggcga ctgctgtgct 300
 38 caagccttcg ccttcatcat gtccctcttt gggctcgcct cgacgctcca gctcttagcc 360
 40 atggccctag agtgctggct gtccctggga cacccttct tctaccagcg gcacatcact 420
 42 gtgcgcgggg gcgtgctcgt ggcgccggct gtgggcgcct tcagcctggc tttctgcgcg 480
 44 ctcccttcg tgggcttcgg gaactttgtg cagtactgtc ccggcacctg gtgtttcttc 540
 46 cagatgatct ccggggacga ctgcgcgtcg gtgaagggt actcgggtgct gtactccacc 600
 48 ctcatggcgc tgttggtgct cgccatcgtg ctgtgcaacc tgggcgcat gcgcaacctc 660
 50 tacaccatgc accagcgct gcgacggcac acgcgctgct gcagcctccg ggaccgcgcg 720
 52 ggcgaggcgt ttccgcaatc cttggaggag ctggaccacc tgctgctgct ggccctcatg 780
 54 accgtgctct tcacatgtg cactctgccg ttagtttatc gcgcttacta tggagcattt 840
 56 aaagctgtcg aagaggagcc cgacgacctc ctageccttg gttttctctc tgtgatttca 900
 58 atcgtggacc cttggatctt tatcattttc agaacttcag tatttcggat gttttttcac 960
 60 aagattttca taagacctct tctttaccga aactggcact gccacttcta ccaaactaac 1020
 62 gtggaatcca gtctgtga 1038
 65 <210> SEQ ID NO: 2
 66 <211> LENGTH: 345
 67 <212> TYPE: PRT
 68 <213> ORGANISM: Cavia porcellus
 70 <400> SEQUENCE: 2
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 73 1 5 10 15

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76 Ser Ala Thr Val Gly Gly Val Leu Phe Ser Ala Gly Leu Leu Gly Asn
77          20          25          30
80 Leu Leu Ala Leu Ala Leu Leu Ala Arg Ser Gly Leu Gly Ser Cys Arg
81          35          40          45
84 Pro Arg Pro Gln Pro Ser Val Phe Tyr Val Leu Val Cys Gly Leu Thr
85          50          55          60
88 Val Thr Asp Leu Leu Gly Lys Cys Leu Val Ser Pro Val Val Leu Ala
89 65          70          75          80
92 Ala Tyr Ala Gln Asn Arg Ser Leu Arg Gly Leu Ala Pro Ala Gln Gly
93          85          90          95
96 Asp Ser Leu Cys Gln Ala Phe Ala Phe Ile Met Ser Phe Phe Gly Leu
97          100          105          110
100 Ala Ser Thr Leu Gln Leu Leu Ala Met Ala Leu Glu Cys Trp Leu Ser
101          115          120          125
104 Leu Gly His Pro Phe Phe Tyr Gln Arg His Ile Thr Val Arg Arg Gly
105          130          135          140
108 Val Leu Val Ala Pro Ala Val Gly Ala Phe Ser Leu Ala Phe Cys Ala
109 145          150          155          160
112 Leu Pro Phe Val Gly Phe Gly Asn Phe Val Gln Tyr Cys Pro Gly Thr
113          165          170          175
116 Trp Cys Phe Phe Gln Met Ile Ser Gly Asp Asp Ser Pro Ser Val Lys
117          180          185          190
120 Gly Tyr Ser Val Leu Tyr Ser Thr Leu Met Ala Leu Leu Val Leu Ala
121          195          200          205
124 Ile Val Leu Cys Asn Leu Gly Ala Met Arg Asn Leu Tyr Thr Met His
125          210          215          220
128 Gln Arg Leu Arg Arg His Thr Arg Cys Cys Ser Leu Arg Asp Arg Ala
129 225          230          235          240
132 Gly Glu Ala Phe Pro Gln Ser Leu Glu Glu Leu Asp His Leu Leu Leu
133          245          250          255
136 Leu Ala Leu Met Thr Val Leu Phe Thr Met Cys Thr Leu Pro Leu Val
137          260          265          270
140 Tyr Arg Ala Tyr Tyr Gly Ala Phe Lys Ala Val Glu Glu Glu Pro Asp
141          275          280          285
144 Asp Leu Leu Ala Leu Arg Phe Leu Ser Val Ile Ser Ile Val Asp Pro
145          290          295          300
148 Trp Ile Phe Ile Ile Phe Arg Thr Ser Val Phe Arg Met Phe Phe His
149 305          310          315          320
152 Lys Ile Phe Ile Arg Pro Leu Leu Tyr Arg Asn Trp His Cys His Phe
153          325          330          335
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161 <211> LENGTH: 21
162 <212> TYPE: DNA
163 <213> ORGANISM: Artificial
165 <220> FEATURE:
166 <223> OTHER INFORMATION: 675_Topo_F3 primer
168 <400> SEQUENCE: 3

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169 gggacaccct ttcttctaca a                                21
172 <210> SEQ ID NO: 4
173 <211> LENGTH: 22
174 <212> TYPE: DNA
175 <213> ORGANISM: Artificial
177 <220> FEATURE:
178 <223> OTHER INFORMATION: 675_Topo_R2 primer
180 <400> SEQUENCE: 4
181 gaacacatgg tgaagagcac tg                                22
184 <210> SEQ ID NO: 5
185 <211> LENGTH: 20
186 <212> TYPE: DNA
187 <213> ORGANISM: Artificial
189 <220> FEATURE:
190 <223> OTHER INFORMATION: 675_GP_3'RACE_F primer
192 <400> SEQUENCE: 5
193 gtgctcgtgg cgccggtgtg                                20
196 <210> SEQ ID NO: 6
197 <211> LENGTH: 25
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial
201 <220> FEATURE:
202 <223> OTHER INFORMATION: 675_Rev_P2 primer
204 <400> SEQUENCE: 6
205 cacatggtga agagcacggt catga                            25
208 <210> SEQ ID NO: 7
209 <211> LENGTH: 28
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial
213 <220> FEATURE:
214 <223> OTHER INFORMATION: 675_RACE_R9 primer
216 <400> SEQUENCE: 7
217 tcaccaggca cttgcctagc aggtctgt                        28
220 <210> SEQ ID NO: 8
221 <211> LENGTH: 39
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial
225 <220> FEATURE:
226 <223> OTHER INFORMATION: GW675 forward primer
228 <400> SEQUENCE: 8
229 aaaagcaggc ttaggaatgt ccttctatcc ctgcaacac            39
232 <210> SEQ ID NO: 9
233 <211> LENGTH: 37
234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial
237 <220> FEATURE:
238 <223> OTHER INFORMATION: GW675 reverse primer
240 <400> SEQUENCE: 9
241 aagaaagctg ggtctcacag actggattcc acgttag              37

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244 <210> SEQ ID NO: 10
245 <211> LENGTH: 9
246 <212> TYPE: PRT
247 <213> ORGANISM: Cavia porcellus
249 <400> SEQUENCE: 10
251 Gln Tyr Cys Pro Gly Thr Trp Cys Arg
252 1 5
255 <210> SEQ ID NO: 11
256 <211> LENGTH: 15
257 <212> TYPE: PRT
258 <213> ORGANISM: Cavia porcellus
260 <400> SEQUENCE: 11
262 Arg Phe Leu Ser Val Ile Ser Ile Val Asp Pro Trp Ile Phe Ile
263 1 5 10 15
266 <210> SEQ ID NO: 12
267 <211> LENGTH: 1080
268 <212> TYPE: DNA
269 <213> ORGANISM: Homo sapiens
271 <400> SEQUENCE: 12
272 atgaagtgcg cgttctaccg ctgccagaac accacctctg tggaaaaagg caactcggcg 60
274 gtgatgggcg ggggtgctctt cagcaccggc ctctctggga acctgctggc cctggggctg 120
276 ctggcgcgct cggggctggg gtggtgctcg cggcgctcac tgcgcccgt gcccctggtc 180
278 ttctacatgc tgggtgtgtgg cctgacggtc accgacttgc tgggcaagtg cctcctaagc 240
280 ccggtggtgc tggctgccta cgctcagaac cggagtctgc ggggtgcttg gcccgcattg 300
282 gacaactcgt tgtgccaagc cttcgccttc ttcatgtcct tctttgggct ctctcgaca 360
284 ctgcaactcc tggccatggc actggagtgc tggtctctcc tagggcacc tttcttctac 420
286 cgacggcaca tcacctgcg cctgggcgca ctggtggccc cgggtggtgag cgccttctcc 480
288 ctggctttct gcgcgtacc tttcatggg ttcggaagt tctgacagta ctgcccggc 540
290 acctggtgct ttatccagat ggtccacgag gagggtctgc tgtcgggtgct ggggtactct 600
292 gtgctctcat ccagctcat ggcgtgctg gtctctgcca ccgtgctgtg caacctcggc 660
294 gccactcgca acctctatgc gatgcacgg cggctgcagc ggcaccgcg ctctgcacc 720
296 agggactgtg ccgagccgcg cgcggacgg agggaagcgt cccctcagcc cctggaggag 780
298 ctggatcacc tctgtgctg ggcgtgatg accgtgctct tctactatgt ttctctgccc 840
300 gtaattttat gcgcttacta tggagcattt aaggatgtca aggagaaaaa caggacctct 900
302 gaagaagcag aagacctcc agccttgcca tttctatctg tgatttcaat tgtggacct 960
304 tggattttta tcattttcag atctccagta tttcgatat tttttcacia gattttcatt 1020
306 agacctctta ggtacaggag ccggtgcagc aattccacta acatggaatc cagtctgtga 1080
309 <210> SEQ ID NO: 13
310 <211> LENGTH: 1074
311 <212> TYPE: DNA
312 <213> ORGANISM: Rattus norvegicus
314 <400> SEQUENCE: 13
315 atgaatgagt cctatcgctg tcaggcagcc acctgggtgg aacggggctc ctacagcgaca 60
317 atgggtggtg tgctcttcag tgcaggactg ctgggcaatc tcttgccgt ggtgctgctg 120
319 gcgcgatccg ggctggggtc ctgccggcca gggccactgc atccgccgcc ctcggtcttt 180
321 tatgtgctag tgtgcggctt gacggtcacc cacttgctgg gcaagtgtct gatcagcccg 240
323 atggtcctgg ctgcctacgc gcaaaatcgg agcctaaagg aactgctgcc tgcctcaggc 300
325 aatcagttat gtgaagcctt cgccttctct atgtccttct ttgggttagc ctgcacctta 360
327 cagctactgg ctatggcact ggagtgtggt ctgtctctgg gacacccttt cttctaccaa 420

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329 aggcacatca cgcggcgccg gggagtgctg gtggcgccag tgcaggcgcc cttctctttg      480
331 gctttctgtg cgctcccctt tgctggcttt gggaggttcg tgcagtactg tccagggtacc      540
333 tgggtgcttca tccagatgat ccacaagaag cgctcattct cggtaatagg cttctctgtg      600
335 ctctactcca gcctcatggc gctgctggtc ctcgcaactg tgggtgtgcaa cctgggtgcc      660
337 atgtccaacc tctatgcat gcacaggcgc cagaggcacc atccccgcgc ctgctccagg      720
339 gaccgcgccc agtcaggctc agactacagg catgggtccc cgaatccttt ggaggagctg      780
341 gaccactttg ttctgctggc tctcacgaca gtgctcttca ccatgtgttc cctgccttta      840
343 atttatcgtg cttactatgg agcctttaa cttgtggaca gagctgacgg agactcggaa      900
345 gacctccaag ccttgcggtt tctgtctgtg atttccatcg tggaccctcg gatcttcac      960
347 attttcagga cttcagatatt ccggatgtta tttcacaagg ctttcacaag acctctgac      1020
349 tacagaaact ggtgcagcca ttcttgccag actaacatgg aatccacttt gtga      1074

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352 <210> SEQ ID NO: 14

353 <211> LENGTH: 1074

354 <212> TYPE: DNA

355 <213> ORGANISM: Mus musculus

357 <400> SEQUENCE: 14

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360 atgggcgctg tgctcttcgg tgcggggctt ctgggcaatc ttctggcgct ggtgctgctg      120
362 ggcgcgctcg gactggggtc ttgccggcca gggccactac acccgccgcc ctcggtcttt      180
364 tatgtgctcg tgtgtggctt gacggtcacc gacttgctgg gcaattgtct gatcagccc      240
366 atggtcctgg ctgcctacgc gcaaaaccag agcctaaagg aactgctgcc tgcctcaggc      300
368 aatcagttat gcgaaacgtt cgccttcctg atgtccttct ttgggctagc ctgcacctta      360
370 cagctggttg ctatggcggt ggagtgtggt ctgtctctgg gacaccctt cttctaccaa      420
372 aggcacgtca ccttgcgccg gggagtgctg gtggcaccgg tctgtggcgc cttctgcttg      480
374 gctttctgtg cgctcccctt tgctgggttt gggaggttcg tgcagtactg tccaggcacc      540
376 tgggtgtttca tccagatgat ccacaaggag cgttcatttt cggtaatagg cttctctgtg      600
378 ctctactcca gcctcatggc gctgctggtc ctcgcaaccg tgggtgtgcaa cctgggtgcc      660
380 atgtacaacc tctatgacat gcacaggcgc cagaggcact atcctcaccg ctgctccagg      720
382 gaccgcgccc agtcaggctc agactacagg cacgggtccc tgcacccctt ggaggagctg      780
384 gaccactttg tgctgtggc tctcatgaca gtgctcttca ccatgtgttc cctgccttta      840
386 atttatcgtg cgtactatgg agcctttaa cttgagaaca aagctgaagg agactcagaa      900
388 gacctccaag ccttgcggtt cctgtctgtg atttccatag tggaccctcg gatcttcac      960
390 atcttcagga cttcagatatt ccggatgtta tttcacaagg ttttcacaag acctctgac      1020
392 tacagaaact ggagcagcca ttcccagcaa agtaacgtgg aatccacttt gtga      1074

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395 <210> SEQ ID NO: 15

396 <211> LENGTH: 359

397 <212> TYPE: PRT

398 <213> ORGANISM: Homo sapiens

400 <400> SEQUENCE: 15

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406 Gly Asn Ser Ala Val Met Gly Gly Val Leu Phe Ser Thr Gly Leu Leu
407          20          25          30
410 Gly Asn Leu Leu Ala Leu Gly Leu Leu Ala Arg Ser Gly Leu Gly Trp
411          35          40          45
414 Cys Ser Arg Arg Pro Leu Arg Pro Leu Pro Ser Val Phe Tyr Met Leu
415          50          55          60
418 Val Cys Gly Leu Thr Val Thr Asp Leu Leu Gly Lys Cys Leu Leu Ser
419 65          70          75          80

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; Xaa Pos. 294,298,347,351

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,18

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L:795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:288

M:341 Repeated in SeqNo=18